NCBI **Blast 2 Sequences results**

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

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BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

Match: 1   Mismatch: -2   gap open: 5   gap extension: 2
x_dropoff: 50   expect: 10.00(wordsize: 11   Filter ☑   [Align]

| Sequence 1 | gi 21361113 | Homo sapiens solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11 (SLC25A11), mRNA | Length 1570 (1 .. 1570) |
| Sequence 2 | gi 3387910 | | Length 1503 (1 .. 1503) |
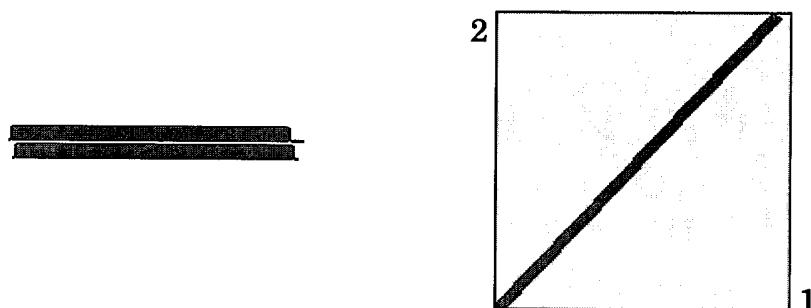
SEQ ALIGNMENT

of 21361113 (seq 1)
& 3387910 (seq 2)

NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence

```
Score = 2832 bits (1473), Expect = 0.0
Identities = 1475/1476 (99%)
 Strand = Plus / Plus
```

```
Query:                        22  ggcgtgcgcgcgccctcgctctgttgcgcgcgcggtgtcaccttgggc
                                   ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:                        11  ggcgtgcgcgcgccctcgctctgttgcgcgcgcggtgtcaccttgggc


Query:                        82  gcgcgcgcacgggacccggagccgagggccattgagtggcgatggcgg
                                   | |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:                        71  gtgcgcgcacgggacccggagccgagggccattgagtggcgatggcgg
2-oxoglutarate carrier protein 1                                     M  A


Query:                       142  ccggggccggcgggatagacgggaagccccgtacctcccctaagtccg
                                   ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:                       131  ccggggccggcgggatagacgggaagccccgtacctcccctaagtccg
2-oxoglutarate carrier protein 7   A  G  A  G  G  I  D  G  K  P  R  T  S  P  K  S
```

```
Query:                              802   tgatcagcggtcttgtcaccactgctgcctccatgcctgtggacattg
                                          ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:                             791   tgatcagcggtcttgtcaccactgctgcctccatgcctgtggacattg
2-oxoglutarate carrier protein     227    M  I  S  G  L  V  T  T  A  A  S  M  P  V  D  I


Query:                              862   tccagaacatgcggatgattgatgggaagccggaatacaagaacgggc
                                          ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:                             851   tccagaacatgcggatgattgatgggaagccggaatacaagaacgggc
2-oxoglutarate carrier protein     247    I  Q  N  M  R  M  I  D  G  K  P  E  Y  K  N  G


Query:                              922   tcaaagttgtccgctacgagggcttcttcagcctgtggaagggcttca
                                          ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:                             911   tcaaagttgtccgctacgagggcttcttcagcctgtggaagggcttca
2-oxoglutarate carrier protein     267    F  K  V  V  R  Y  E  G  F  F  S  L  W  K  G  F


Query:                              982   cccgcctgggcccccacaccgtcctcaccttcatcttcttggagcaga
                                          ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:                             971   cccgcctgggcccccacaccgtcctcaccttcatcttcttggagcaga
2-oxoglutarate carrier protein     287    A  R  L  G  P  H  T  V  L  T  F  I  F  L  E  Q


Query:                             1042   acaagcgtctcttcctcagtggctgaagcggccggggggctcccactcg
                                          |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:                            1031   acaagcgtctcttcctcagtggctgaagcggccggggggctcccactcg
2-oxoglutarate carrier protein     307    Y  K  R  L  F  L  S  G  ^^^


Query:                             1102   atagccactgcgccctgggggcctgggctctgctgccctggacccctc
                                          ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:                            1091   atagccactgcgccctgggggcctgggctctgctgccctggacccctc


Query:                             1162   ttccacagtgtggtttcttcctctgcggtaaaggacttggtctgttct
                                          ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:                            1151   ttccacagtgtggtttcttcctctgcggtaaaggacttggtctgttct


Query:                             1222   agcttgccctgctcgtcctgatcctgtgatttctctgtccttggctat
                                          ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:                            1211   agcttgccctgctcgtcctgatcctgtgatttctctgtccttggctat


Query:                             1282   ctggaaaacttcctgaggatttctggcctccccctgggttttagtttc
                                          ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:                            1271   ctggaaaacttcctgaggatttctggcctccccctgggttttagtttc


Query:                             1342   acagcagaagatcccctttgtcagtggggaaaccaaggcagagctgag
                                          ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:                            1331   acagcagaagatcccctttgtcagtggggaaaccaaggcagagctgag


Query:                             1402   agcagaagccatcaagatggtcaaagggcctgcagagggagatgtggc
                                          ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:                            1391   agcagaagccatcaagatggtcaaagggcctgcagagggagatgtggc
```

```
Query:              1462 tcattgaggacttaataaattggattgatgacacca 1497
                         ||||||||||||||||||||||||||||||||||||
Sbjct:              1451 tcattgaggacttaataaattggattgatgacacca 1486
```

CPU time: 0.08 user secs.   0.03 sys. secs   0.11 total secs.

```
Lambda       K       H
   1.33    0.621      1.12

Gapped
Lambda       K       H
   1.33    0.621      1.12
```

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 8
Number of Sequences: 0
Number of extensions: 8
Number of successful extensions: 1
Number of sequences better than 10.0: 1
length of query: 1570
length of database: 7,833,321,048
effective HSP length: 25
effective length of query: 1545
effective length of database: 7,833,321,023
effective search space: 12102480980535
effective search space used: 12102480980535
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)

```

**Ӯ NCBI** **Blast 2 Sequences results**

PubMed        Entrez        BLAST        OMIM        Taxonomy        Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

Matrix BLOSUM62 ▼ gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.00 wordsize: 3 Filter ☑ Align

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**Sequence 1** lcl|seq_1 **Length** 314 (1 .. 314)

**Sequence 2** lcl|seq_2 **Length** 314 (1 .. 314)



NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

```
Score = 622 bits (1603), Expect = e-177
Identities = 314/314 (100%), Positives = 314/314 (100%)
```

```
Query: 1    MAATASAGAGGIDGKPRTSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTRE 60
            MAATASAGAGGIDGKPRTSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTRE
Sbjct: 1    MAATASAGAGGIDGKPRTSPKSVKFLFGGLAGMGATVFVQPLDLVKNRMQLSGEGAKTRE 60
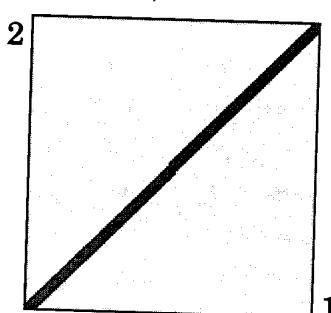
Query: 61   YKTSFHALTSILKAEGLRGIYTGLSAGLLRQATYTTTRLGIYTVLFERLTGADGTPPGFL 120
            YKTSFHALTSILKAEGLRGIYTGLSAGLLRQATYTTTRLGIYTVLFERLTGADGTPPGFL
Sbjct: 61   YKTSFHALTSILKAEGLRGIYTGLSAGLLRQATYTTTRLGIYTVLFERLTGADGTPPGFL 120

Query: 121  LKAVIGMTAGATGAFVGTPAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTL 180
            LKAVIGMTAGATGAFVGTPAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTL
Sbjct: 121  LKAVIGMTAGATGAFVGTPAEVALIRMTADGRLPADQRRGYKNVFNALIRITREEGVLTL 180

Query: 181  WRGCIPTMARAVVVNAAQLASYSQSKQFLLDSGYFSDNILCHFCASMISGLVTTAASMPV 240
            WRGCIPTMARAVVVNAAQLASYSQSKQFLLDSGYFSDNILCHFCASMISGLVTTAASMPV
Sbjct: 181  WRGCIPTMARAVVVNAAQLASYSQSKQFLLDSGYFSDNILCHFCASMISGLVTTAASMPV 240

Query: 241  DIAKTRIQNMRMIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFTPYYARLGPHTVLTFIFL 300
            DIAKTRIQNMRMIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFTPYYARLGPHTVLTFIFL
Sbjct: 241  DIAKTRIQNMRMIDGKPEYKNGLDVLFKVVRYEGFFSLWKGFTPYYARLGPHTVLTFIFL 300

Query: 301  EQMNKAYKRLFLSG 314
            EQMNKAYKRLFLSG
Sbjct: 301  EQMNKAYKRLFLSG 314
```

Alignment of aa encoded by① NM_003562 (SEQ1) and ② AAF070548 (SEQ10 NO2) 100% ...

CPU time: 0.09 user secs.   0.02 sys. secs   0.11 total secs.

Lambda   K   H
  0.323   0.138   0.404

Gapped
Lambda   K   H
  0.267   0.0410   0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 1236
Number of Sequences: 0
Number of extensions: 82
Number of successful extensions: 9
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 314
length of database: 422,818,587
effective HSP length: 126
effective length of query: 188
effective length of database: 422,818,461
effective search space: 79489870668
effective search space used: 79489870668
T: 9
A: 40
X1: 16 (7.5 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (22.0 bits)
S2: 74 (33.1 bits)